

WHAT IS CLAIMED IS:

1                   1.       A method for identifying a monomer domain that binds to a target  
2 molecule, the method comprising,  
3                   providing a library of monomer domains, wherein the monomer domains each  
4 bind an ion;  
5                   screening the library of monomer domains for affinity to a first target  
6 molecule; and  
7                   identifying at least one monomer domain that binds to at least one target  
8 molecule.

1                   2.       The method of claim 1, wherein the ion is selected from calcium or  
2 zinc.

1                   3.       The method of claim 1, wherein the monomer domain is selected from  
2 the group consisting of an A domain, EGF domain, EF Hand, Cadherin domain, C-type  
3 lectin, C2 domain, Annexin, Gla-domain, Trombospondin type 3 domain and zinc finger.

1                   4.       The method of claim 1, further comprising linking the identified  
2 monomer domains to a second monomer domain to form a library of multimers, each  
3 multimer comprising at least two monomer domains;  
4                   screening the library of multimers for the ability to bind to the first target  
5 molecule; and  
6                   identifying a multimer that binds to the first target molecule.

1                   5.       The method of claim 1, wherein the monomer domains are between 25  
2 and 500 amino acids.

1                   6.       The method of claim 1, wherein each monomer domain of the selected  
2 multimer binds to the same target molecule.

1                   7.       The method of claim 1, wherein the selected multimer comprises at  
2 least three monomer domains.

1                   8.       The method of claim 1, wherein the selected multimer comprises four  
2 monomer domains.

1                    9.        The method of claim 4, comprising identifying a multimer with an  
2 improved avidity for the target compared to the avidity of a monomer domain alone.

1                    10.       The method of claim 1, wherein the monomer domain is an LDL  
2 receptor class A domain monomer comprising the following sequence:

3                     $C_aX_{3-15}C_bX_{3-15}C_cX_{6-7}C_d(D,N)X_4C_eX_{4-6}DEX_{2-8}C_f$

4                    wherein C is cysteine,  $X_{n-m}$  represents between n and m number of  
5 independently selected amino acids, and (D,N) indicates that the position can be either D or  
6 N; and

7                    wherein  $C_a-C_c$ ,  $C_b-C_e$  and  $C_d-C_f$  form disulfide bonds.

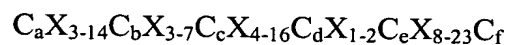
1                    11.       The method of claim 10, wherein the monomer domain is an LDL  
2 receptor class A domain monomer comprising the following sequence:

3                     $CaX_{6-7}CbX_{4-5}CcX_6CdX_5CeX_{8-10}Cf$

4                    wherein X is defined as follows:



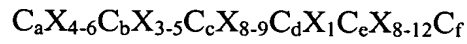
12. The method of claim 1, wherein the monomer domain is an EGF domain monomer comprising the following sequence:



wherein C is cysteine,  $X_{n-m}$  represents between n and m number of independently selected amino acids; and

wherein  $C_a$ - $C_c$ ,  $C_b$ - $C_e$  and  $C_d$ - $C_f$  form disulfide bonds.

13. The method of claim 10, wherein the monomer domain is an EGF domain monomer comprising the following sequence:



wherein X is defined as follows:

X(4,6)				X(3,5)			X(8,9)								X(1)		X(8,12)							
X1	X2	X3	X4	X1	X2	X3	X1	X2	X3	X4	X5	X6	X7	X8	X1	X1	X1	X2	X3	X4	X5	X6	X7	X8
A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
D	D	D	E	D	D	E	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E
F	G	G	G	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F	F
G	H	H	H	G	H	H	G	H	H	H	H	H	H	H	G	H	H	H	H	H	H	H	H	H
H	I	K	K	I	K	K	I	K	K	K	K	K	K	K	I	K	K	K	K	K	K	K	K	K
I	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L
L	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
M	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
N	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P
P	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
Q	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
S	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
T	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V	V
V	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W
W	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
Y																								

14. The method of claim 1, further comprising a step of mutating at least one monomer domain, thereby providing a library comprising mutated monomer domains.

- 1                   15.     The method of claim 14, wherein the mutating step comprises  
2     recombining a plurality of polynucleotide fragments of at least one polynucleotide encoding a  
3     polypeptide domain.
- 1                   16.     The method of claim 14, wherein the mutating step comprises directed  
2     evolution.
- 1                   17.     The method of claim 14, wherein the mutating step comprises site-  
2     directed mutagenesis.
- 1                   18.     The method of claim 1, further comprising,  
2                   screening the library of monomer domains for affinity to a second target  
3     molecule;  
4                   identifying a monomer domain that binds to a second target molecule;  
5                   linking at least one monomer domain with affinity for the first target molecule  
6     with at least one monomer domain with affinity for the second target molecule, thereby  
7     forming a multimer with affinity for the first and the second target molecule.
- 1                   19.     The method of claim 1, wherein the target molecule is selected from  
2     the group consisting of a viral antigen, a bacterial antigen, a fungal antigen, an enzyme, an  
3     enzyme substrate, a cell surface protein, an enzyme inhibitor, a reporter molecule, and a  
4     receptor.
- 1                   20.     The method of claim 1, wherein the library of monomer domains is  
2     expressed as a phage display, ribosome display or cell surface display.
- 1                   21.     The method of claim 1, wherein the library of monomer domains is  
2     presented on a microarray.
- 1                   22.     The method of claim 1, wherein the monomer domains form a  
2     secondary structure by the formation of disulfide bonds.
- 1                   23.     The method of claim 1, wherein the monomer domains are linked by a  
2     polypeptide linker.
- 1                   24.     The method of claim 23, wherein the polypeptide linker is a linker  
2     naturally-associated with the monomer domain.

1                    25.     The method of claim 23, wherein the polypeptide linker is a variant of  
2     a linker naturally-associated with the monomer domain.

1                    26.     The method of claim 23, wherein the linker is between 1-20 amino  
2     acids.

1                    27.     The method of claim 23, wherein the linker comprises the following  
2     sequence, A<sub>1</sub>A<sub>2</sub>A<sub>3</sub>A<sub>4</sub>A<sub>5</sub>A<sub>6</sub>, wherein

3                    A<sub>1</sub> is selected from the amino acids A, P, T, Q, E and K;

4                    A<sub>2</sub> and A<sub>3</sub> are any amino acid except C, F, Y, W, or M;

5                    A<sub>4</sub> is selected from the amino acids S, G and R;

6                    A<sub>5</sub> is selected from the amino acids H, P, and R

7                    A<sub>6</sub> is the amino acid, T.

1                    28.     A method of producing a polypeptide comprising the monomer domain  
2     identified in claim 1.

1                    29.     The method of claim 28, wherein the polypeptide is produced by  
2     recombinant gene expression.

1                    30.     A polypeptide comprising the monomer domain identified in claim 1.

1                    31.     A polynucleotide encoding the monomer domain identified in claim 1.

1                    32.     A method for identifying a multimer that binds to at least one target  
2     molecule, the method comprising:

3                    providing a library of multimers, wherein each multimer comprises at least  
4     two monomer domains and each monomer domain exhibits a binding specificity for a target  
5     molecule; and

6                    screening the library of multimers for target molecule-binding multimers.

1                    33.     The method of claim 32, further comprising identifying target  
2     molecule-binding multimers having an avidity for the target molecule that is greater than the  
3     avidity of a single monomer domain for the target molecule.

1                    34.     The method of claim 32, wherein one or more of the multimers  
2     comprises a monomer domain that specifically binds to a second target molecule.

1                   35.     A method of producing a polypeptide comprising the multimer  
2 identified in claim 32.

1                   36.     The method of claim 35, wherein the polypeptide is produced by  
2 recombinant gene expression.

1                   37.     A method for identifying a multimer that binds to a target molecule,  
2 the method comprising,  
3                   providing a library of monomer domains and/or immuno domains;  
4                   screening the library of monomer domains and/or immuno domain for affinity  
5 to a first target molecule; and  
6                   identifying at least one monomer domain and/or immuno domain that binds to  
7 at least one target molecule;  
8                   linking the identified monomer domain and/or immuno domain to a library of  
9 monomer domains and/or immuno domains to form a library of multimers, each multimer  
10 comprising at least two monomer domains, immuno domains or combinations thereof;  
11                  screening the library of multimers for the ability to bind to the first target  
12 molecule; and  
13                  identifying a multimer that binds to the first target molecule.

1                   38.     The method of claim 37, wherein the monomer domains each bind an  
2 ion.

1                   39.     The method of claim 38, wherein the ion is selected from the group  
2 consisting of calcium and zinc.

1                   40.     The method of claim 37, wherein the monomer domains are selected  
2 from the group consisting of an A domain, EGF domain, EF Hand, Cadherin domain, C-type  
3 lectin, C2 domain, Annexin, Gla-domain, Trombospondin type 3 domain and zinc finger.

1                   41.     A library of multimers, wherein  
2 each multimer comprises at least two monomer domains connected by a  
3 linker; and  
4 each monomer domain binds an ion.

1                   42..    The library of claim 41, wherein the ion is selected from calcium and  
2    zinc.

1                   43.    The library of claim 41, wherein each monomer domain of the  
2    multimers is a non-naturally occurring monomer domain.

1                   44.    The library of claim 41, wherein the monomer domains are between 25  
2    and 500 amino acids.

1                   45.    The library of claim 41, wherein the polypeptide domains are selected  
2    from the group consisting of consisting of an A domain, EGF domain, EF Hand, Cadherin  
3    domain, C-type lectin, C2 domain, Annexin, Gla-domain, Trombospondin type 3 domain and  
4    zinc finger.

1                   46.    The library of claim 41, wherein the monomer domain is an LDL  
2    receptor class A domain monomer comprising the following sequence:

3                    $C_aX_{3-15}C_bX_{3-15}C_cX_{6-7}C_d(D,N)X_4C_eX_{4-6}DEX_{2-8}C_f$

4                   wherein C is cysteine,  $X_{n-m}$  represents between n and m number of  
5    independently selected amino acids, and (D,N) indicates that the position can be either D or  
6    N; and

7                   wherein  $C_a-C_e$ ,  $C_b-C_e$  and  $C_d-C_f$  form disulfide bonds.

1                   47.    The library of claim 46, wherein the monomer domain is an LDL  
2    receptor class A domain monomer comprising the following sequence:

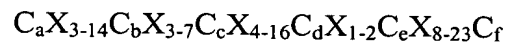
3                    $CaX_{6-7}C_bX_{4-5}C_cX_6C_dX_5C_eX_{8-10}C_f$

4                   wherein X is defined as follows:



C	X(6,7)						C	X(4,5)				C	X(6)						C	X(5)					C	X(8,10)								C	
	X1	X2	X3	X4	X5	X6		X1	X2	X3	X4		X1	X2	X3	X4	X5	X6		X1	X2	X3	X4	X5		X1	X2	X3	X4	X5	X6	X7	X8		
	A	A	A	A	A	A		A	A		A		A	A	A	A	A	A		A	A	A				A	A	A	A	A	A	A	A		
	D	D	D	D				D	D	D	D		D	D	D	D	D		D	D	D	D			D	D	D	D	D	D	D	D	D		
	E	E	E	E		E		E	E	E	F		E	E	E	E			E	E	E	E			E	E	E	E	E	E	E	E	E		
	F	F	F	F		F		F	F	F	F		F	F	F	F			F	F	F				F	F	F	F	F	F	F	F	F		
	G	G	G	G				G	G	G	G		G	G	G	G			G	G	G			G	G	G	G	G	G	G	G	G	G		
	H	H	H	H		H		H	H	H			H	H	H		H		H	H	H	H			H	H	H	H	H	H	H	H	H		
	I	I	I	I				I	I	I	I		I	I	I		I		I	I	I			I	I	I	I	I	I	I	I	I	I		
	K	K	K	K		K		K	K	K	K		K	K	K	K			K	K	K			K	K	K	K	K	K	K	K	K	K		
	L	L	L	L		L		L	L	L	L		L	L	L	L			L	L	L			L	L	L	L	L	L	L	L	L	L		
	M	M	M	M		M		M	M	M	M		M	M	M	M			M	M	M			M	M	M	M	M	M	M	M	M	M		
	N	N	N	N		N		N	N	N	N		N	N	N	N			N	N	N	N			N	N	N	N	N	N	N	N	N	N	
	P	P	P	P		P		P	P	P	P		P	P	P	P			P	P	P	P			P	P	P	P	P	P	P	P	P		
	Q	Q	Q	Q		Q		Q	Q	Q	Q		Q	Q	Q	Q			Q	Q	Q	Q			Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	
	R	R	R	R		R		R	R	R	R		R	R	R	R			R	R	R	R			R	R	R	R	R	R	R	R	R	R	
	S	S	S	S		S		S	S	S	S		S	S	S	S			S	S	S	S			S	S	S	S	S	S	S	S	S	S	
	T	T	T	T		T		T	T	T	T		T	T	T	T			T	T	T	T			T	T	T	T	T	T	T	T	T	T	
	V	V	V	V		V		V	V	V	V		V	V	V	V			V	V	V	V			V	V	V	V	V	V	V	V	V	V	
	W	W	W	W		W		W	W	W	W		W	W	W	W			W	W	W	W			W	W	W	W	W	W	W	W	W	W	
	Y	Y	Y	Y		Y		Y	Y	Y	Y		Y	Y	Y	Y			Y	Y	Y	Y			Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	
	X1	X2	X3	X4	X5	X6	X7	X1	X2	X3	X4	X5								X1	X2	X3	X4	X5	X6	X7	X8	X9							
	A	A					A	A	A	A	A									A	A	A			A	A	A	A							
	D	D	D	D				D	D	D	D									D						D	D	D	D	D	D	D	D		
	E	E		E	E		E	E	E	E	E									E	E	E			E	E	E	E	E	E	E	E	E		
	F	F	F	F		F		F	F	F																									
	G	G	G	G		G		G	G	G	G									G	G				G	G	G	G	G	G	G	G	G		
	H	H		H		H		H	H	H	H									H	H				H	H	H	H	H	H	H	H	H		
	K		K	K		K		K	K	K	K																								
	L	L	L	L		L		L	L	L	L									L	L				L	L	L	L	L	L	L	L	L		
	M			M		M		M	M	M	M														M	M	M	M	M	M	M	M	M	M	
	N	N	N	N		N		N	N	N	N									N	N				N	N	N	N	N	N	N	N	N	N	
	P	P	P	P		P		P	P	P	P									P	P				P	P	P	P	P	P	P	P	P	P	
	Q		Q	Q		Q		Q	Q	Q	Q									Q	Q				Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	
	R	R	R	R		R		R	R	R	R									R	R				R	R	R	R	R	R	R	R	R	R	
	S	S	S	S		S		S	S	S	S									S	S				S	S	S	S	S	S	S	S	S	S	
	T	T	T	T		T		T	T	T	T									T	T				T	T	T	T	T	T	T	T	T	T	
	V	V	V	V		V		V	V	V	V									V	V				V	V	V	V	V	V	V	V	V	V	
	W					W		W	W	W	W									W	W				W	W	W	W	W	W	W	W	W	W	
	Y					Y		Y	Y	Y	Y									Y	Y				Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	
	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10										X1	X2	X3	X4	X5	X6	X7	X8	X9	X10						
	A									A										A	A	A	A	A	A	A	A	A							
	D	D		D						D										D	D	D	D	D	D	D	D	D							
	E		F		E					E										E	E	E	E	E	E	E	E	E							
	G		G																																
	H		H																	H	H				H	H	H	H	H	H	H	H	H		
	I		I																	I	I				I	I	I	I	I	I	I	I	I		
	K		K																	K	K				K	K	K	K	K	K	K	K	K		
	L			L																L	L				L	L	L	L	L	L	L	L	L		
	M																			M	M				M	M	M	M	M	M	M	M	M	M	
	N		N																	N	N				N	N	N	N	N	N	N	N	N	N	
	P		P																	P	P				P	P	P	P	P	P	P	P	P	P	
	Q		Q																	Q	Q				Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	
	R		R																	R	R				R	R	R	R	R	R	R	R	R	R	
	S		S																	S	S				S	S	S	S	S	S	S	S	S	S	
	T		T																	T	T				T	T	T	T	T	T	T	T	T	T	
	V		V																	V	V				V	V	V	V	V	V	V	V	V	V	
	W																			W	W				W	W	W	W	W	W	W	W	W	W	
	Y																			Y	Y				Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	

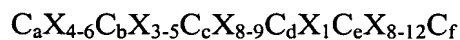
48. The library of claim 41, wherein the monomer domain is an EGF domain monomer comprising the following sequence:



wherein C is cysteine,  $X_{n-m}$  represents between n and m number of independently selected amino acids; and

wherein  $C_a$ - $C_c$ ,  $C_b$ - $C_e$  and  $C_d$ - $C_f$  form disulfide bonds.

49. The library of claim 48, wherein the monomer domain is an EGF domain monomer comprising the following sequence:



wherein X is defined as follows:

C	X(4,6)				C	X(3,5)			C	X(8,9)								C	X(1)	C	X(8/12)								C	
	X1	X2	X3	X4		X1	X2	X3		X1	X2	X3	X4	X5	X6	X7	X8		X1		X1	X2	X3	X4	X5	X6	X7	X8		
	A	A	A	A		A				A	A			A	A	A	A		A		A	A	A	A	A	A	A		A	A
	D	D	D			D		D		D	D			D	D	D		D		D	D		D	D	D	D		D	D	
	E	E	E	E		E		E	F	E	F			E	F	F		E		E	F		E	F	F	F		E	F	
	F					F	G	H		F	G	H		F	G	H		F		F	G	H		F	G	H		F	G	
	G	H	H	G		G	H	H		G	H	H		G	H	H		G		H	H		G	H	H	H		H	H	
	H					H				H				H				H		H								H		
	I	K	K	K		K				K	K	K	K	K	K	L		K		K	K		K	K	K	K		K	K	
	L	L	L			L	L			L	L	L	L	L	L	L		L		L	L		L	L	L	L		L	L	
	M	M	M	M		M				M	M	M	M	M	M	M		M		M	M		M	M	M	M		M	M	
	N	N	N	N		N	N	N		N	N	N	N	N	N	N		N		N	N		N	N	N	N		N	N	
	P	P	P	P		P				P	P	P	P	P	P	P		P		P	P		P	P	P	P		P	P	
	Q	Q	R	R		Q	Q	Q	R	Q	Q	R	R	Q	Q	R		Q		Q	R	R	Q	R	R	Q		Q	R	
	R	S	T	T		R	S	T	T	R	S	T	T	R	S	T		R		R	S	T	T	S	R	S		R	S	
	S	T	T			S	T			S	T			S	T			S		S								S		
	T	T				T				T				T				T		T								T		
	V					V				V				V				V		V								V		
	W			W		W				W				W	W	W		W		W				W				W		
	Y			Y		Y	Y			Y	Y			Y	Y	Y		Y		Y	Y		Y	Y			Y	Y		

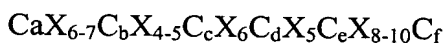
C	X1	X2	X3	X4	X5	C	X1	X2	X3	X4	C	X1	X2	X3	X4	X5	X6	X7	X8	X9	C	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	C
	A	A	A	A	A		A	A	A	A		A	A	A	A	A	A	A		A		A	A		A	A	A	A	A	A	A	A	A	
	D	E					D	E				D	E				D	E					D	E				D	E				D	E
	E	F	F	F			E	F	F			E	F	F			E	F					E	F	F	F		E	F	F	F		E	F
	G				F		G					G					G						G					G					G	
	H						H					H					H						H					H					H	
	I	K					I	K				I	K				I	K					I	K				I	K				I	K
	L	L	L				L	L	L			L	L	L			L	L	L				L	L	L			L	L	L			L	L
	M			N			M			N		M			N		M			N			M			N		M			N		M	
	N	P	P	P			N	P	P	P		N	P	P	P		N	P	P	P			N	P	P	P		N	P	P	P		N	P
	Q	R	R	R			Q	R	R	R		Q	R	R	R		Q	R	R	R			Q	R	R	R		Q	R	R	R		Q	R
	R	S	T	T			R	S	T	T		R	S	T	T		R	S	T	T			R	S	T	T		R	S	T	T		R	S
	S	T					S	T				S	T				S	T					S	T				S	T				S	T
	T				W		T					T					T						T					T					T	
	V			Y			V					V					V						V					V					V	
	W			Y			W					W					W						W					W					W	
	Y			Y			Y					Y					Y						Y					Y					Y	

C	X1	X2	X3	X4	X5	X6	C	X1	X2	X3	X4	X5	X6	X7	X8	C
	A	A	A	A	A	A		A	C							
	D	D	D	D	D	D		D	E							
	E	F	F	F	F	F		E	F	F						
	G							G	H	H						
	H							H	I							
	I	K	K	K	K	K		I	K	L						
	L	L	L	L	L	L		L	M							
	M	N	N	N	N	N		M								
	N	P	P	P	P	P		N	P							
	Q	R	R	R	R	R		Q	R	Q						
	R	S	T	T	T	T		R	S	T						
	S	T			W			S	T							
	T				Y			T								
	V				Y			V								
	W				Y			W								
	Y				Y			Y								

50. The library of claim 41, wherein the monomer domains are linked by a polypeptide linker.

- 1                    51.     The library of claim 50, wherein the linker is between 1-20 amino acid  
2 residues.
- 1                    52.     The library of claim 50, wherein the polypeptide linker is naturally  
2 associated with the monomer domain.
- 1                    53.     The library of claim 41, wherein the monomer domains form a  
2 secondary structure by the formation of disulfide bonds.
- 1                    54.     The library of claim 53, wherein the multimers comprise an A domain  
2 connected to a monomer domain by a polypeptide linker.
- 1                    55.     The library of claim 54, wherein the linker comprises the following  
2 sequence,  $A_1A_2A_3A_4A_5A_6$ , wherein  
3                     $A_1$  is selected from the amino acids A, P, T, Q, E and K;  
4                     $A_2$  and  $A_3$  are any amino acid except C, F, Y, W, or M;  
5                     $A_4$  is selected from the amino acids S, G and R;  
6                     $A_5$  is selected from the amino acids H, P, and R  
7                     $A_6$  is the amino acid, T.
- 1                    56.     A polypeptide comprising at least two monomer domains separated by  
2 a heterologous linker, wherein each monomer domain specifically binds to a target molecule  
3 and each monomer domain binds an ion.
- 1                    57.     The polypeptide of claim 56, wherein the ion is selected from calcium  
2 and zinc.
- 1                    58.     The polypeptide of claim 56, wherein the monomer domain is an LDL  
2 receptor class A domain monomer comprising the following sequence:  
3                     $C_aX_{3-15}C_bX_{3-15}C_cX_{6-7}C_d(D,N)X_4C_eX_{4-6}DEX_{2-8}C_f$   
4                    wherein C is cysteine,  $X_{n-m}$  represents between n and m number of  
5 independently selected amino acids, and (D,N) indicates that the position can be either D or  
6 N; and  
7                    wherein  $C_a-C_c$ ,  $C_b-C_e$  and  $C_d-C_f$  form disulfide bonds.

59. The polypeptide of claim 58, wherein the monomer domain is an LDL receptor class A domain monomer comprising the following sequence:



wherein X is defined as follows:

C		X(6,7)					C		X(4,5)				C		X(6)						C		X(5)					C		X(8,10)										C	
		X1	X2	X3	X4	X5	X6			X1	X2	X3	X4			X1	X2	X3	X4	X5	X6			X1	X2	X3	X4	X5	X6	X7	X8										
		A	A	A	A	A	A			A	A			A	C			A	A	A				A	A	A			A	A											
		D	E	D	D		E			D	D		D	E	F			D	D	D	D				D	D	D	D		D	D	D	D	D							
		F	F	F	F	F	F			F	F	G	G	F	F			F	F	F	F	F			F	F	F	F	E	F	F	F	F	F							
		G	H	G	H	G	H			G	H	G	H	H	G			G	H	G	H	G			G	H	G	H	G	G	H	G	H	G	H						
		K	K	K	K	K	K			K					I			K	K	K	K	K			K	K	K	K		K	K	K	K	K	K						
		L	L	L	L	L	L			L			L	L	L			L	L	L	L	L			L	L	L	L	L	L	L	L	L	L	L						
		M	M	M	M	M	M			M			M	M	M			M	M	M	M	M			M	M	M	M	M	M	M	M	M	M	M						
		N	N	N	N	N	N			N	N		N	N	N			N	N	N	N	N			N	N	N	N	N	N	N	N	N	N	N	N					
		P	Q	Q	Q	Q	Q			P	Q	Q	Q	Q	Q			P	Q	Q	Q	Q			P	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q					
		R	R	R	R	R	R			R	R	R	R	R	R			R	R	R	R	R			R	R	R	R	R	R	R	R	R	R	R	R					
		S	T	T	T	T	T			S	T	T	T	T	T			S	T	T	T	T			S	T	T	T	T	T	T	T	T	T	T	T					
		V								V								V							V																
		W	W	W						W	W	W						W	W	W	W	W			W	W	W	W	W	W	W	W	W	W	W	W					
		Y	Y	Y	Y					Y	Y							Y	Y	Y	Y	Y			Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y					

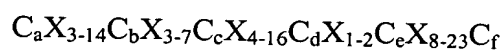
C		X(6,7)						C		X(4,5)				C		X(6)						C		X(5)					C		X(8,10)										C	
		X1	X2	X3	X4	X5	X6	X7			X1	X2	X3	X4	X5			X1	X2	X3	X4	X5	X6			X1	X2	X3	X4	X5	X6	X7	X8									
		A	A					A			A	A	A	A	A			A	A	A	A	A			A	A	A			A	A	A	A									
		D	E	D	D	D	D	E			D	E	D	D	D			D	E	D	D	D			D	D	D	D	D	D	D	D	D	D	D	D						
		F	F	F	F	F	F				F	F	F	F	F			F	F	F	F	F			F	F	F	F	F	F	F	F	F	F	F	F						
		G	G	G	G	G	G				G	G	G	G	G			G	G	G	G	G			G	G	G	G	G	G	G	G	G	G	G	G						
		H	H					H			H	H						H	H						H	H																
		K						K			K							K							K																	
		L	L					L			L							L	L						L	L																
		M						M			M							M							M																	
		N	N					N			N	N						N	N						N	N																
		P	P					P			P	P	Q	Q	Q			P	P						P	P																
		Q	Q					Q			Q	Q	Q	Q	Q			Q	Q						Q	Q																
		R	R					R			R	R	R	R	R			R	R						R	R																
		S	T					S			S	T	T	T	T			S	T						S	T																
		T						T			T							T							T																	
		V						V			V							V							V																	
		W						W			W	W	W	W	W			W	W						W	W																
		Y						Y			Y							Y							Y																	

C		X(6,7)						C		X(4,5)				C		X(6)						C		X(5)					C		X(8,10)										C	
		X1	X2	X3	X4	X5	X6	X7			X1	X2	X3	X4	X5			X1	X2	X3	X4	X5	X6			X1	X2	X3	X4	X5	X6	X7	X8	X9								
		A	A					A			A	A	A	A	A			A	A	A	A	A			A	A	A			A	A	A	A									
		D	E	D	D	D	D	E			D	E	D	D	D			D	E	D	D	D			D	D	D	D	D	D	D	D	D	D	D	D						
		F	F	F	F	F	F				F	F	F	F	F			F	F	F	F	F			F	F	F	F	F	F	F	F	F	F	F	F						
		G	G	G	G	G	G				G	G	G	G	G			G	G	G	G	G			G	G	G	G	G	G	G	G	G	G	G	G						
		H	H					H			H	H						H	H						H	H																
		K						K			K							K							K																	
		L	L					L			L							L	L						L	L																
		M						M			M							M							M																	
		N	N					N			N	N						N	N						N	N																
		P	P					P			P	P	Q	Q	Q			P	P						P	P																
		Q	Q					Q			Q	Q	Q	Q	Q			Q	Q						Q	Q																
		R	R					R			R	R	R	R	R			R	R						R	R																
		S	T					S			S	T	T	T	T			S	T						S	T																
		T						T			T							T							T																	
		V						V			V							V							V																	
		W						W			W	W	W	W	W			W	W						W	W																
		Y						Y			Y							Y							Y																	

C		X(6,7)						C		X(4,5)				C		X(6)						C		X(5)					C		X(8,10)										C	
		X1	X2	X3	X4	X5	X6	X7			X1	X2	X3	X4	X5			X1	X2	X3	X4	X5	X6			X1	X2	X3	X4	X5	X6	X7	X8	X9	X10							
		A	A					A			A	A	A	A	A			A	A	A	A	A			A	A	A			A	A	A	A									
		D	E	D	D	D	D	E			D	E	D	D	D			D	E	D	D	D			D	D	D	D	D	D	D	D	D	D	D	D						
		F	F	F	F	F	F				F	F	F	F	F			F	F	F	F	F			F	F	F	F	F	F	F	F	F	F	F	F						
		G	G	G	G	G	G				G	G	G	G	G			G	G	G	G	G			G	G	G	G	G	G	G	G	G	G	G	G						
		H	H					H			H	H						H	H						H	H																
		K						K			K							K							K																	
		L	L					L			L							L	L						L	L																
		M						M			M							M							M																	
		N	N					N			N	N						N	N						N	N																
		P	P					P			P	P	Q	Q	Q			P	P						P	P																
		Q	Q					Q			Q	Q	Q	Q	Q			Q	Q						Q	Q																
		R	R					R			R	R	R	R	R			R	R						R	R																
		S	T					S			S	T	T	T	T			S	T						S	T																
		T						T			T							T							T																	
		V						V			V							V							V																	
		W						W			W	W	W	W	W			W	W						W	W																
		Y						Y			Y							Y							Y																	

C		X(6,7)						C		X(4,5)				C		X(6)						C		X(5)					C		X(8,10)										C	
		X1	X2	X3	X4	X5	X6	X7			X1	X2	X3	X4	X5			X1	X2	X3	X4	X5	X6			X1	X2	X3	X4	X5	X6	X7	X8	X9	X10							
		A	A					A			A	A	A	A	A	</																										

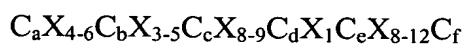
60. The polypeptide of claim 56, wherein the monomer domain is an EGF domain monomer comprising the following sequence:



wherein C is cysteine,  $X_{n-m}$  represents between n and m number of independently selected amino acids; and

wherein  $C_a-C_c$ ,  $C_b-C_e$  and  $C_d-C_f$  form disulfide bonds.

61. The polypeptide of claim 60, wherein the monomer domain is an EGF domain monomer comprising the following sequence:



wherein X is defined as follows:

C	X(4,6)				C	X(3,5)			C	X(8,9)								C	X(1)	C	X(8/12)								C
	X1	X2	X3	X4		X1	X2	X3		X1	X2	X3	X4	X5	X6	X7	X8		X1		X1	X2	X3	X4	X5	X6	X7	X8	
A	A	A	A	A		A		A		A	A	A	A	A	A	A	A		A		A	A	A	A	A	A	A	A	
D	D	D				D		D		D	D	D	D	D		D	D		D		D	D	D	D	D	D	D	D	
E	E	E	E	E		E		E		E	E	E	E	E		E	E		E		E	E	E	E	E	E	E	E	
F						F		F		F	F	F	F	F		F	F		F		F	F	F	F	F	F	F	F	
G	G	G	G	G		G		G		G	G	G	G	G		G	G		G		G	G	G	G	G	G	G	G	
H	H	H				H		H		H	H	H	H	H		H	H		H		H	H	H	H	H	H	H	H	
I						I		I		I	I	I	I	I		I	I		I		I	I	I	I	I	I	I	I	
K	K	K				K		K		K	K	K	K	K		K	K		K		K	K	K	K	K	K	K	K	
L	L	L				L		L		L	L	L	L	L		L	L		L		L	L	L	L	L	L	L	L	
M										M	M	M	M	M		M	M				M	M	M	M	M	M	M	M	
N	N	N	N	N		N		N		N	N	N	N	N		N	N		N		N	N	N	N	N	N	N	N	
P	P	P	P	P		P		P		P	P	P	P	P		P	P		P		P	P	P	P	P	P	P	P	
Q	Q	Q	Q	Q		Q		Q		Q	Q	Q	Q	Q		Q	Q		Q		Q	Q	Q	Q	Q	Q	Q	Q	
R	R	R	R	R		R		R		R	R	R	R	R		R	R		R		R	R	R	R	R	R	R	R	
S	S	S	S	S		S		S		S	S	S	S	S		S	S		S		S	S	S	S	S	S	S	S	
T	T	T	T	T		T		T		T	T	T	T	T		T	T		T		T	T	T	T	T	T	T	T	
V						V		V		V	V	V	V	V		V	V		V		V	V	V	V	V	V	V	V	
W										W	W	W	W	W		W	W				W	W	W	W	W	W	W	W	
Y	Y	Y	Y	Y		Y		Y		Y	Y	Y	Y	Y		Y	Y		Y		Y	Y	Y	Y	Y	Y	Y	Y	

C	X(4,6)					C	X(3,5)				C	X(8,9)									C	X(1)	C	X(8/12)												C
	X1	X2	X3	X4	X5		X1	X2	X3	X4		X1	X2	X3	X4	X5	X6	X7	X8	X9		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12			
A	A	A	A	A	A		A	A	A	A		A	A	A	A	A	A	A	A	A		A	A	A	A	A	A	A	A	A	A	A				
D	D				D		D			D	D	D	D	D		D	D		D		D	D	D	D	D	D	D	D	D	D	D	D				
E	E	E	E	E	F		E	E	F		E	E	E	E		E	E		E		E	E	E	E	E	E	E	E	E	E	E	E				
F	F	F	F	F	G		F	F	G		F	F	F	F		F	F		F		F	F	F	F	F	F	F	F	F	F	F	F				
G	G	H	H	H	I		G	H	I		G	H	H			G			G		G	H	H	H	H	H	H	H	H	H	H	H				
I	I	K	K	L	K		I	K	L		I	K	L			I			I		I	K	K	K	K	K	K	K	K	K	K	K				
K	K	L	L	L	M		K	L	L		K	L	L			K			K		K	L	L	L	L	L	L	L	L	L	L	L				
L	L	M	M	M	N		L	M	N		L	M	N			L			L		L	M	M	M	M	M	M	M	M	M	M	M				
M	M	N	N	N	P		M	N	P		M	N	P			M			M		M	N	N	N	N	N	N	N	N	N	N	N				
N	N	P	P	P	Q		N	P	Q		N	P	Q			N			N		N	P	P	P	P	P	P	P	P	P	P	P				
P	P	Q	Q	Q	R		P	Q	R		P	Q	R			P			P		P	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q				
Q	Q	R	R	R	S		Q	R	S		Q	R	S			Q			Q		Q	R	R	R	R	R	R	R	R	R	R	R				
R	R	S	S	S	T		R	S	T		R	S	T			R			R		R	S	S	S	S	S	S	S	S	S	S	S				
S	S	T	T	T	V		S	T	V		S	T	V			S			S		S	T	T	T	T	T	T	T	T	T	T	T				
T	T	V	V	V	W		T	V	V		T	V	V			T			T		T	V	V	V	V	V	V	V	V	V	V	V				
V	V	W	W	W	Y		V	W	Y		V	W	Y			V			V		V	W	W	W	W	W	W	W	W	W	W	W				
W	W	Y	Y	Y			W	Y			W	Y				W			W		W	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y				

1                   62.     The polypeptide of claim 56, wherein each monomer domain is a non-  
2 naturally occurring protein monomer domain.

1                   63.     The polypeptide of claim 56, wherein the polypeptide comprises a first  
2 monomer domain that binds a first target molecule and a second monomer domain that binds  
3 a second target molecule.

1                   64.     The polypeptide of claim 56, wherein the polypeptide comprises two  
2 monomer domains, each monomer domain having a binding specificity for a different site on  
3 a first target molecule.

1                   65.     The polypeptide of claim 56, wherein the monomer domains are  
2 between 25 and 500 amino acids.

1                   66.     The polypeptide of claim 56, wherein the polypeptide comprises at  
2 least three monomer domains.

1                   67.     The polypeptide of claim 56, wherein the polypeptide comprises four  
2 monomer domains.

1                   68.     The polypeptide of claim 56, comprising polypeptide has an improved  
2 avidity for a target molecule compared to the avidity of a monomer domain alone.

1                   69.     The polypeptide of claim 68, wherein the avidity of the polypeptide is  
2 at least two times the avidity of a monomer domain alone.

1                   70.     The polypeptide of claim 56, wherein the monomer domain is selected  
2 from the group consisting of an A domain, EGF domain, EF Hand, Cadherin domain, C-type  
3 lectin, C2 domain, Annexin, Gla-domain, Trombospondin type 3 domain and zinc finger.

1                   71.     The polypeptide of claim 56, wherein the target molecule is selected  
2 from the group consisting of a viral antigen, a bacterial antigen, a fungal antigen, an enzyme,  
3 a cell surface protein, an enzyme inhibitor, a reporter molecule, and a receptor.

1                   72.     The polypeptide of claim 73, wherein the domains form a secondary  
2 structure by the formation of disulfide bonds.

1                    73.     The polypeptide of claim 56, wherein the monomer domains are linked  
2 by a polypeptide linker.

1                    74.     The polypeptide of claim 73, wherein the polypeptide linker is a  
2 naturally-occurring linker associated with the monomer domain.

1                    75.     The polypeptide of claim 73, wherein the linker is between 1-20 amino  
2 acids.

1                    76.     The polypeptide of claim 73, wherein the linker comprises the  
2 following sequence,  $A_1A_2A_3A_4A_5A_6$ , wherein

3                     $A_1$  is selected from the amino acids A, P, T, Q, E and K;

4                     $A_2$  and  $A_3$  are any amino acid except C, F, Y, W, or M;

5                     $A_4$  is selected from the amino acids S, G and R;

6                     $A_5$  is selected from the amino acids H, P, and R

7                     $A_6$  is the amino acid, T.

1                    77.     A method for identifying a human chimeric monomer domain that  
2 binds to a target molecule, said method comprising:

3                    providing a sequence alignment of at least two naturally occurring human  
4 monomer domains from the same family of monomer domains;

5                    identifying amino acid residues in corresponding positions in the human  
6 monomer domain sequences that differ between the human monomer domains;

7                    generating a library of human chimeric monomer domains, wherein each  
8 human chimeric monomer domain sequence consists of amino acid residues that correspond  
9 in type and position to residues from two or more naturally occurring human monomer  
10 domains from the same family of monomer domains;

11                    screening the library of human chimeric monomer domains for binding to a  
12 target molecule; and

13                    identifying a human chimeric monomer domain that binds to a target  
14 molecule.

1                    78.     The method of claim 77 wherein the naturally occurring human  
2 monomer domains are LDL receptor A-domain monomers.

1                   79.     The method of claim 77 wherein the naturally occurring human  
2 monomer domains are EGF-like domain monomers.

1                   80.     The method of claim 77 wherein the screening of the library is carried  
2 out using a two-hybrid screening method.

1                   81.     A method of producing a polypeptide comprising the multimer  
2 identified in claim 77.

1                   82.     The method of claim 82, wherein the polypeptide is produced by  
2 recombinant gene expression.

1                   83.     A non-naturally-occurring polypeptide comprising an LDL receptor  
2 class A domain monomer, wherein the monomer comprises the following sequence:

3                    $C_aX_{3-15}C_bX_{3-15}C_cX_{6-7}C_d(D,N)X_4C_eX_{4-6}DEX_{2-8}C_f$

4                   wherein C is cysteine,  $X_{n-m}$  represents between n and m number of  
5 independently selected amino acids, and (D,N) indicates that the position can be either D or  
6 N; and

7                   wherein  $C_a-C_c$ ,  $C_b-C_e$  and  $C_d-C_f$  form disulfide bonds.

1                   84.     The polypeptide of claim 83, wherein the monomer domain is an LDL  
2 receptor class A domain monomer comprising the following sequence:

3                    $CaX_{6-7}CbX_{4-5}CcX_6CdX_5CeX_{8-10}Cf$

4                   wherein X is defined as follows:



X(6,7)							X(4,5)				X(6)						X(5)					X(8,10)									
X1	X2	X3	X4	X5	X6		X1	X2	X3	X4		X1	X2	X3	X4	X5	X6		X1	X2	X3	X4	X5	X1	X2	X3	X4	X5	X6	X7	X8
A	A	A	A	A	A		A	A			A	A	A	A	A		A	A	A				A	A	A	A					
C																															
D	D	D	D				D	D	D	D									D	D	D	D		D	D			D	D		
E	E	E	E	E		E	E	E	E	F								E	E	E	E	E		E	E	F	F	F	F		
F	F	F	F	F	F		F	F	F	F	F	F	F	F	F			F	F	F	F	F									
G	G	G	G				G	G	G	G	G	G	G					G	G	G	G		G	G	G						
H	H	H	H	H	H		H	H	H		H							H	H	H	H	H									
I											I																				
K	K	K	K	K	K		K		K	K	K	K	K	K				K	K	K			K		K	L	L	L	L		
L	L			L	L		L		L	L	L	L	L	L				L	L	L			L	L	L	L	L	L	L	L	
M	M										M	M	M	M	M			M	M				M	M	M	M	M	M	M	M	
N	N	N	N			N	N	N	N		N	N	N	N	N			N	N	N	N	N		N	N	N	N	N	N	N	
P	P	P				P	P				P	P	P					P				P						P			
Q	Q	Q	Q	Q	Q		Q	Q	Q	Q	Q	Q	Q	Q				Q	Q	Q	Q	Q		Q	Q			Q	Q		
R	R	R	R	R	R		R	R	R	R	R	R	R	R				R	R	R	R	R		R	R	R	R	R	R	R	
S	S	S	S	S	S		S	S	S	S	S	S	S	S				S	S	S	S	S		S	S	S	S	S	S	S	
T	T	T	T	T	T		T	T	T	T	T	T	T	T				T	T	T	T	T		T	T	T	T	T	T	T	
V	V	V				V	V				V	V	V	V	V			V	V	V			V	V				V			
W	W	W				W					W	W	W	W	W			W	W	W			W	W				W			
Y	Y	Y	Y			Y	Y				Y	Y	Y	Y	Y			Y	Y				Y	Y				Y			

X1	X2	X3	X4	X5	X6	X7	X1	X2	X3	X4	X5
A	A					A	A	A	A	A	
D	D	D	D	D			D	D	D	D	D
E	E	E	E	E		E	E	E	E	E	
F	F	F	F		F		F				
G	G	G	G	G		G	G	G	G	H	
H	H				H		H	H	H		
K		K	K	K		K	K	K	K	K	
L	L	L			L		L		L	L	
M				M		M					
N	N	N	N	N		N	N	N	N	N	
P	P	P	Q		P		P	P	P	Q	
R	R	R	R	R	R		R	R	R	R	
S	S	T	T	T			S	S	S	T	
T							T	T	T	T	
V	V	V				V	V				
W						W					
Y						Y	Y				

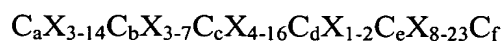
X1	X2	X3	X4	X5	X6	X7	X8	X9
A		A				A	A	A
D	D				D		D	D
E		F			E	E	E	E
F		G	H			G	G	
G								H
L	M					L	M	L
N						N	N	N
P		Q				P	P	Q
S		R				S		S
T			S	T				
V							V	
Y		Y						Y

X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
			A			A	A	A	A
D	D			D		D	D	D	
E		F		E		E	E	E	E
G		G	H			G		H	H
K	K							K	K
L		L				L	M	L	L
N	N					N	N	N	N
P						P	P	P	P
Q	Q	R	S			Q	R	Q	R
R	R	S	S			R	S	S	T
S	S			T					
W						W			
Y								Y	Y

- 5
- 1 85. The polypeptide of claim 83, wherein the polypeptide is 65 or fewer
- 2 amino acids long.
- 1 86. The polypeptide of claim 83, wherein the monomer is fused to a
- 2 heterologous amino acid sequence.
- 1 87. The polypeptide of claim 83, wherein the monomer binds to a target
- 2 molecule.

1                    88.     The polypeptide of claim 86, wherein the heterologous amino acid  
2     sequence is selected from an affinity peptide, a heterologous LDL receptor class A domain, a  
3     heterologous EGF domain, a purification tag, an enzyme, and a reporter protein.

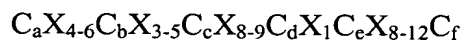
1                    89.     A non-naturally-occurring polypeptide comprising an EGF domain  
2     monomer, wherein the EGF domain monomer comprises the following sequence:



4                    wherein C is cysteine,  $X_{n-m}$  represents between n and m number of  
5     independently selected amino acids; and

6                    wherein  $C_a-C_c$ ,  $C_b-C_e$  and  $C_d-C_f$  form disulfide bonds.

1                    90.     The polypeptide of claim 89, wherein the monomer domain is an EGF  
2     domain monomer comprising the following sequence:



4                    wherein X is defined as follows:

C X(4,6)					C X(3,5)			C X(8,9)								C X(1)		C X(8/12)								C	
X1	X2	X3	X4		X1	X2	X3	X1	X2	X3	X4	X5	X6	X7	X8	X1		X1	X2	X3	X4	X5	X6	X7	X8		
A	A	A	A		A		A	A	A	A	A	A	A	A	A	A		A	A	A		A	A				
D	D	D			D		D	D	D	D	D	D	D	D	D	D		D	D	D		D	D				
E	E	E	E		E		E	E	E	E	E	E	E	E	E	E		E	E	E		E	E				
F	F	F	F		F		F	F	F	F	F	F	F	F	F	F		F	F	F		F	F				
G	G	G	G		G		G	G	G	G	G	G	G	G	G	G		G	G	G		G	G				
H	H	H			H		H	H	H	H	H	H	H	H	H	H		H	H	H		H	H				
I	I	I			I		I	I	I	I	I	I	I	I	I	I		I	I	I		I	I				
K	K	K			K		K	K	K	K	K	K	K	K	K	K		K	K	K		K	K				
L	L	L			L		L	L	L	L	L	L	L	L	L	L		L	L	L		L	L				
M	M	M	M				M	M	M	M	M	M	M	M	M	M		M	M	M		M	M				
N	N	N	N		N		N	N	N	N	N	N	N	N	N	N		N	N	N		N	N				
P	P	P	P		P		P	P	P	P	P	P	P	P	P	P		P	P	P		P	P				
Q	Q	Q	Q		Q		Q	Q	Q	Q	Q	Q	Q	Q	Q	Q		Q	Q	Q		Q	Q				
R	R	R	R		R		R	R	R	R	R	R	R	R	R	R		R	R	R		R	R				
S	S	S	S		S		S	S	S	S	S	S	S	S	S	S		S	S	S		S	S				
T	T	T	T		T		T	T	T	T	T	T	T	T	T	T		T	T	T		T	T				
V	V	V	V		V		V	V	V	V	V	V	V	V	V	V		V	V	V		V	V				
W		W						W	W	W	W	W	W	W	W	W		W									
Y	Y		Y		Y		Y	Y	Y	Y	Y	Y	Y	Y	Y	Y		Y	Y	Y		Y	Y				

X1	X2	X3	X4	X5
A	A	A	A	A
D	D		D	
E	E	E	F	
F	F	F		
G	G	G	G	
H	H	H		
I	I	I	I	
K	K	L	L	
L	L	M	N	
M	M	N	P	
N	N	P	Q	
P	P	Q	R	
Q	Q	R	S	
R	R	S	T	
S	S	T	V	
T	T	V	W	
V		W	Y	
W		Y		
Y			Y	

X1	X2	X3	X4
A	A	A	A
D	D		D
E	E		F
F	F	G	
G	G		
H	H		H
I	I		I
K	K		K
L	L		L
M	M		M
N	N		N
P	P		P
Q	Q		Q
R	R		R
S	S		S
T	T		T
V			V
W			W
Y			Y

X1	X2	X3	X4	X5	X6	X7	X8	X9
A	A	A	A	A	A	A	A	A
D	D	D	D	D	D	D		E
E	E	E	E	E	E	E		
F	F	F	F	F	F	F		F
G	G	G	G	G	G	G		
H	H	H						H
I	I							I
K	K							K
L	L							L
M	M							M
N	N							N
P	P							P
Q	Q							Q
R	R							R
S	S							S
T	T							T
V	V							V
W								W
Y	Y							Y

X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
A	A		A	A	A	A	A	A		A	A
D	D	D	D	D		D	D	D		D	D
E	E	E	E	E		E	E	E		E	E
F	F	F	F	F		F	F	F		F	F
G	G	G	G	G		G	G	G		G	G
H	H		H	H		H	H	H		H	H
I	I		I	I		I	I	I		I	I
K	K		K	K		K	K	K		K	K
L	L		L	L		L	L	L		L	L
M	M		M	M		M	M	M		M	M
N	N		N	N		N	N	N		N	N
P	P		P	P		P	P	P		P	P
Q	Q		Q	Q		Q	Q	Q		Q	Q
R	R		R	R		R	R	R		R	R
S	S		S	S		S	S	S		S	S
T	T		T	T		T	T	T		T	T
V	V		V	V		V	V	V		V	V
W			W	W		W	W	W		W	W
Y			Y	Y		Y	Y	Y		Y	Y

X1	X2	X3	X4	X5	X6	X7	X8
A	A	A	A	A	A	A	A
D	D	D	D	D			
E	E	E	E	E			
F	F	F	F	F			
G	G	G	G	G			
H	H	H	H	H			
I	I	I	I	I			
K	K	K	K	K			
L	L	L	L	L			
M	M	M	M	M			
N	N	N	N	N			
P	P	P	P	P			
Q	Q	Q	Q	Q			
R	R	R	R	R			
S	S	S	S	S			
T	T	T	T	T			
V	V	V	V	V			
W							
Y	Y	Y					

X1	X2	X3	X4	X5	X6	X7	X8
A	A	A	A	A	A	A	A
D	D	D	D	D			
E	E	E	E	E			
F	F	F	F	F			
G	G	G	G	G			
H	H	H	H	H			
I	I	I	I	I			
K	K	K	K	K			
L	L	L	L	L			
M	M	M	M	M			
N	N	N	N	N			
P	P	P	P	P			
Q	Q	Q	Q	Q			
R	R	R	R	R			
S	S	S	S	S			
T	T	T	T	T			
V	V	V	V	V			
W							
Y	Y	Y					

- 5
- 1 91. The polypeptide of claim 89, wherein the EGF domain monomer is
- 2 fused to a heterologous amino acid sequence.
- 1 92. The polypeptide of claim 89, wherein the monomer binds to a target
- 2 molecule.
- 1 93. The polypeptide of claim 89, wherein the polypeptide is 45 or fewer
- 2 amino acids long.

1                    94.     The polypeptide of claim 91, wherein the heterologous amino acid  
2     sequence is selected from an affinity peptide), a heterologous LDL receptor class A domain, a  
3     heterologous EGF domain, a purification tag, an enzyme, and a reporter protein.